

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Regents of the University of Minnesota

(ii) TITLE OF THE INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
- (B) STREET: 3100 Norwest Center, 90 South 7th Street
- (C) CITY: Minneapolis
- (D) STATE: MN
- (E) COUNTRY: USA
- (F) ZIP: 55402

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US97/22228
- (B) FILING DATE: 05-DEC-1997
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/032,930
- (B) FILING DATE: 06-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Skoog, Mark T
- (B) REGISTRATION NUMBER: 40,178
- (C) REFERENCE/DOCKET NUMBER: 600.346WOI1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 612-332-5300
- (B) TELEFAX: 612-332-9081
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCATCACGGG TGGATTCTTG AACACAGGTG

29

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCATCACGCC CCCCGTCGAC GATAAAATAG TTGCTAAGCT ACAAGCT

47

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAAATA CAATACATAT GTAATAATAA TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA ATTTCCATAA ATATTAATAA ATAATTAAGA ATAAAATAAT AAATAATTAA TC	60
	120
	172

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA TAAATATATA AATAAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA ATTCATCAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	60 120 172
---	------------------

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA TAAATATATA AATAAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA ATTCATCAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	60 120 172
---	------------------

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA TAAATATATA AATAAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA ATTCATCAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	60 120 172
---	------------------

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCATCACCAT CACCAAGAAG AAATAATTAC ATATTAATAA CAATACATAT GTAATAATAA	60
TAAATATATA AATAAAATAA TTACATATTA AAAATAATAC TTAATTATAA AAACACTATA	120
ATTTCCATAA ATATTAATAA ATAATTAAAA ATAAAATAAT AAATAATTAA TC	172

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCATCACGGG TGGATCCTTG AACAGGTGC A	31
-----------------------------------	----

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 828...1580
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCATCACGCA	TCACTCATGT	TTGACAGCTT	ATCATCGATA	AGCTTACTTT	TCGAATCAGG	60
TCTATCCTTG	AAACAGGTGC	AACATAGATT	AGGGCATGGA	GATTTACCAAG	ACAACATATGA	120
ACGTATATAC	TCACATCACG	CAATCGGAA	TTGATGACAT	TGGAACCTAAA	TTCAATCAAT	180
TTGTTACTAA	CAAGCAACTA	GATTGACAAC	TAATTCTCAA	CAAACGTTAA	TTTAACAAACA	240
TTCAAGTAAC	TCCCACCAGC	TCCATCAATG	CTTACCGTAA	GTAATCATAA	CTTACTAAAAA	300
CCTTGTACCA	TCAAGGTTTT	TTCTTTTGT	CTTGTTCATG	AGTACCCATA	ACTTTCTATA	360
TTATTGACAA	CTAAATTGAC	AACTCTTCAA	TTATTTTCT	GTCTACTCAA	AGTTTTCTTC	420
ATTTGATATA	GTCTAATTCC	ACCATCACTT	CTTCCACTCT	CTCTACCGTC	ACAACCTCAT	480
CATCTCTCAC	TTTTCGTGT	GGTAACACAT	AATCAAATAT	CTTCCCGTTT	TTACGCACTA	540
TCGCTACTGT	GTCACCTAAA	ATATACCCCT	TATCAATCGC	TTCTTTAAAC	TCATCTATAT	600
ATAACATATT	TCATCCTCCT	ACCTATCTAT	TCGTAAAAG	ATAAAAATAA	CTATTGTTT	660
TTTTGTTATT	TTATAATAAA	ATTATTAATA	TAAGTTAACG	TTTTTAAAAA	ATATACAATT	720
TTATTCTATT	TATAGTTAGC	TATTTTTCA	TTGTTAGTAA	TATTGGTCAA	TTGTAATAAC	780
CTTTTAAAT	CTAGAGGAGA	ACCCAGATAT	AAAATGGAGG	AATATTA	ATG GAA AAC	836
				Met	Glu Asn	
				1		

AAT AAA AAA GTA TTG AAG AAA ATG GTA TTT TTT GTT TTA GTG ACA TTT	884
Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu Val Thr Phe	
5 10 15	

CTT GGA CTA ACA ATC TCG CAA GAG GTA TTT GCT CAA CAA GAC CCC GAT	932
Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln Asp Pro Asp	
20 25 30 35	

CCA AGC CAA CTT CAC AGA TCT AGT TTA GTT AAA AAC CTT CAA AAT ATA Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile 40 45 50	980
TAT TTT CTT TAT GAG GGT GAC CCT GTT ACT CAC GAG AAT GTG AAA TCT Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser 55 60 65	1028
GTT GAT CAA CTT TTA TCT CAC CAT TTA ATA TAT AAT GTT TCA GGG CCA Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro 70 75 80	1076
AAT TAT GAT AAA TTA AAA ACT GAA CTT AAG AAC CAA GAG ATG GCA ACT Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr 85 90 95	1124
TTA TTT AAG GAT AAA AAC GTT GAT ATT TAT GGT GTA GAA TAT TAC CAT Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His 100 105 110 115	1172
CTC TGT TAT TTA TGT GAA AAT GCA GAA AGG AGT GCA TGT ATC TAC GGA Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly 120 125 130	1220
GGG GTA ACA AAT CAT GAA GGG AAT CAT TTA GAA ATT CCT AAA AAG ATA Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile 135 140 145	1268
GTC GTT AAA GTA TCA ATC GAT GGT ATC CAA AGC CTA TCA TTT GAT ATT Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile 150 155 160	1316
GAA ACA AAT AAA AAA ATG GTA ACT GCT CAA GAA TTA GAC TAT AAA GTT Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val 165 170 175	1364
AGA AAA TAT CTT ACA GAT AAT AAG CAA CTA TAT ACT AAT GGA CCT TCT Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser 180 185 190 195	1412

AAA TAT GAA ACT GGA TAT ATA AAG TTC ATA CCT AAG AAT AAA GAA AGT Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu Ser 200 205 210	1460
TTT TGG TTT GAT TTT TTC CCT GAA CCA GAA TTT ACT CAA TCT AAA TAT Phe Trp Phe Asp Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr 215 220 225	1508
CTT ATG ATA TAT AAA GAT AAT GAA ACG CTT GAC TCA AAC ACA AGC CAA Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln 230 235 240	1556
ATT GAA GTC TAC CTA ACA ACC AAG TAACTTTTG CTTTGGCAA CCTTACCTAC Ile Glu Val Tyr Leu Thr Thr Lys 245 250	1610
TGCTGGATTT AGAAATTTA TTGCAATTCT TTTATTAATG TAAAAACCGC TCATTTGATG AGCGGTTTG TCTTATCTAA AGGAGCTTA CCTCCTAACG CTGCAAAATT TTAAATGTTG GATTTTGTA TTTGTCTATT GTATTTGATG GGTAATCCA TTTTCGACA GACATCGTCG TGCCACCTCT AACACCAAAA TCATAGACAG GAGCTTGTAG CTTAGCAACT ATTTTATCGT C	1670 1730 1790 1850 1851

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Glu	Asn	Asn	Lys	Lys	Val	Leu	Lys	Met	Val	Phe	Phe	Val	Leu	
1				5				10					15		
Val	Thr	Phe	Leu	Gly	Leu	Thr	Ile	Ser	Gln	Glu	Val	Phe	Ala	Gln	Gln
				20				25					30		
Asp	Pro	Asp	Pro	Ser	Gln	Leu	His	Arg	Ser	Ser	Leu	Val	Lys	Asn	Leu
				35				40				45			
Gln	Asn	Ile	Tyr	Phe	Leu	Tyr	Glu	Gly	Asp	Pro	Val	Thr	His	Glu	Asn
				50			55				60				
Val	Lys	Ser	Val	Asp	Gln	Leu	Leu	Ser	His	His	Leu	Ile	Tyr	Asn	Val
	65				70				75			80			
Ser	Gly	Pro	Asn	Tyr	Asp	Lys	Leu	Lys	Thr	Glu	Leu	Lys	Asn	Gln	Glu
				85				90				95			
Met	Ala	Thr	Leu	Phe	Lys	Asp	Lys	Asn	Val	Asp	Ile	Tyr	Gly	Val	Glu
				100				105			110				
Tyr	Tyr	His	Leu	Cys	Tyr	Leu	Cys	Glu	Asn	Ala	Glu	Arg	Ser	Ala	Cys
				115				120			125				
Ile	Tyr	Gly	Gly	Val	Thr	Asn	His	Glu	Gly	Asn	His	Leu	Glu	Ile	Pro
				130			135			140					
Lys	Lys	Ile	Val	Val	Lys	Val	Ser	Ile	Asp	Gly	Ile	Gln	Ser	Leu	Ser
	145				150				155			160			
Phe	Asp	Ile	Glu	Thr	Asn	Lys	Met	Val	Thr	Ala	Gln	Glu	Leu	Asp	
				165				170			175				
Tyr	Lys	Val	Arg	Lys	Tyr	Leu	Thr	Asp	Asn	Lys	Gln	Leu	Tyr	Thr	Asn
				180				185			190				
Gly	Pro	Ser	Lys	Tyr	Glu	Thr	Gly	Tyr	Ile	Lys	Phe	Ile	Pro	Lys	Asn
				195				200			205				
Lys	Glu	Ser	Phe	Trp	Phe	Asp	Phe	Phe	Pro	Glu	Pro	Glu	Phe	Thr	Gln
				210			215			220					
Ser	Lys	Tyr	Leu	Met	Ile	Tyr	Lys	Asp	Asn	Glu	Thr	Leu	Asp	Ser	Asn
	225				230				235			240			
Thr	Ser	Gln	Ile	Glu	Val	Tyr	Leu	Thr	Thr	Lys					
				245				250							